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TITLE OF THE INVENTION

A34 AND A33-LIKE 3 DNA, PROTEINS, ANTIBODIES THERETO AND METHODS OF TREATMENT USING SAME

FIELD OF THE INVENTION

[0001] The invention relates to A34 and A33-like 3 polypeptides, and to the nucleotide sequences encoding these polypeptides, and nucleotide and polypeptide fragments thereof, as well as antisense sequences thereof. The invention also relates to immunoglobulin products that bind with specificity to A34 antigen and/or A33-like 3 antigen, and CDR and variable regions thereof. This invention is also directed to methods of inhibiting cancer in a patient with such immunoglobulin products, and to compositions comprising such immunoglobulin products, as well as to kits and methods of detecting cancers.

BACKGROUND OF THE INVENTION

[0002] Modern medicine has been indisputably enriched by the intersection of traditional treatments for disease with the inroads of molecular biology. In particular, immunology has provided new hope for the treatment of various diseases, particularly neoplastic diseases, by providing well-characterized and specific antibodies. Antibodies have become important as therapeutic agents because they may be targeted to a specific site for action. For example, cancer cells may possess a "marker" protein that may be a binding site or antigen for a particular antibody.

[0003] Historically, antibodies were generated in laboratory animals (usually mice or rabbits) by injecting laboratory animals with the antigen of interest over an extended period. (For general discussion of the structure and biosynthesis of immunoglobulins, see standard immunology textbooks, such as W.E. Paul, *Fundamental Immunology*, Raven Press, New York, NY

1993, or Janeway et al., *Immunobiology The Immune System In Health and Disease*, Garland Publishing, New York, NY 2001.) The foreign antigen resulted in an immune response; the resulting antibodies could then be purified from blood. However, this approach has limitations. *In vivo* use of antibodies from a different species may induce a potentially fatal response (for example, murine antibodies when injected into humans may produce a human anti-mouse antibody response- the "HAMA" response, see, for example, Schiff et al., *Cancer Research* 45: 879-885 (1985)). Additionally, non-human antibodies will be less efficacious in stimulating human complement or cell mediated toxicity.

[0004] Molecular biology again begins to provide an answer to these issues. Chimeric and recombinant antibodies are now being used to address these issues. Chimeric antibodies exploit the component nature of immunoglobulin products by combining portions of antibodies from different species. For example, the variable region from a mouse may be combined with the constant regions from a human. Recombinant DNA techniques are then used for cutting and splicing the various components to form functional immunoglobulin products. Another approach for expanding the utility of antibodies into immunoglobulin products is the technique known as "CDR grafting." In this method, only the complementarity determining region, "CDR," is inserted into a human antibody framework. Even this approach may be fine-tuned by substitution of critical murine antibody residues in the human variable regions. The binding of an antibody to its target antigen is mediated through the complementarity-determining regions (CDRs) of its heavy and light chains, with the role of CDR3 of the heavy chain being of particular importance (Xu and Davis, Immunity, 13:37-45, 2000). The use and production of such humanized antibodies continues to be explored, but these techniques are in common current usage. U.S. Patent Nos. 5,225,539; 5,530,101; 5,585,089; and 5,859,205 describe examples of such techniques.

[0005] Yet another approach to avoid the potential problems of immunogenic reactions against non-human protein sequences is using fully

human antibodies. Methods for preparing fully human antibodies are well known in the art. For example, fully human antibodies can be prepared by immunizing transgenic mice which express human immunoglobulins instead of mouse immunoglobulins. An antibody response in such a mouse directly generates fully human antibodies. Examples of such mice include the Xenomouse™ (Abgenix, Inc.) and the HuMAb-Mouse@ (Medarex, Inc.,), see also U.S. Patents No. 6,207,418, No. 6,150,584, No. 6,111,166, No. 6,075,181, No. 5,922,545, No. 5,545,806 and No. 5,569,825. Antibodies can then be prepared by standard techniques, e.g., standard hybridoma techniques, or by phage display (see below). These antibodies will then contain only fully human amino acid sequences.

[0006] Monoclonal antibodies, including fully human antibodies, may also be generated and isolated from phage display libraries. The construction and screening of phage display libraries are well known in the art, see, e.g., Marks et al., *J. Mol. Biol.* 222(3): 581-597 (1991); Hoogenboom et al., *J. Mol. Biol.*, 227(2): 381-388 (1992); and U.S. Patent Nos. 5,885,793, and 5,969,108.

[0007] The following references are illustrative of such fully human antibodies and phage display techniques: Marks et al., "By-passing immunization. Human antibodies from V-gene libraries displayed on phage," *J. Mol. Biol.* 222(3):581-597 (1991); Hoogenboom et al., "By-passing immunisation. Human antibodies from synthetic repertoires of germline VH gene segments rearranged in vitro," *J. Mol. Biol.* 227(2):381-388 (1992).

[0008] Novel strategies for improving the efficacy of therapeutic monoclonal antibodies, such as augmenting their *in vivo* effector function, conjugating them directly to cytotoxic agents or radionuclides, and activating such conjugated agents with pre-targeted pro-drugs, as well as coupling monoclonal antibody therapy with traditional chemotherapy regimes, have been introduced. Large scale clinical trials employing these second generation monoclonal antibodies are currently underway and some have gained FDA approval for the treatment of cancer, most notably anti-c-erbB-2/Her2neu (Herceptin) for the treatment of breast cancer, anti-CD20

(Rituxan) for the treatment of non-Hodgkins lymphoma, and anti-CD52 (Campath) for the treatment B cell chronic lymphocytic leukemia.

[0009] The discovery of new, therapeutically relevant cell surface target molecules has not kept pace with the rapid advances in monoclonal antibody technology, and only a relatively small number of antigenic targets are being pursued in this regard. This is especially poignant given the momentous progress in gene discovery emanating from the analysis of the human genome, trascriptome, and proteome. In contrast, the identification of intracellular targets for active-specific cancer immunotherapy i.e., cancer vaccines, has flourished in the last decade. Thus, mining the human transcriptome for new cell surface antigens is highly warranted. In this regard, the instant invention resulted partially from searching the human expressed sequence tag (EST) database for novel transcripts encoding tissue-restricted cell surface proteins because these may represent new targets for monoclonal antibody based therapies.

[0010] The A33/JAM gene family includes at least seven previously known proteins (A33, CAR, HCTX, ELAM, JAM1, JAM2, and JAM3). These proteins are generally distinguished by two transmembrane domains (with a single signal sequence) and two Ig-like domains. One member, A33, is known to be associated with colon cancer. The isolation and characterization of the A33 molecule is described in U.S. Patent No. 5,712,369. Humanized antibodies to A33 are described in U.S. Patent No. 5,958,412;; 6,307,026, and Rader et al., *J. Biol. Chem.* 275(18):13668-76 (2000); methods of using A33 antibodies are described in U.S. Patent Nos. 6,346,249 B1 and 6,342,587. All these references are specifically incorporated herein by reference.

[0011] Human clinical trials have been conducted with mouse and humanized antibodies directed to A33. The biodistribution and imaging characteristics of ^{131}I-mAb A33 were studied in colon carcinoma patients with hepatic metastases. The studies showed that mAb A33 localization was antigen-specific, cancer:liver ratios were 2.3- to 45 fold higher for specific

antibody as compared to non-specific antibodies. See, for example, Welt et al., *J. Clin. Oncol.* 8:1894-1906 (1990). A subsequent radioimmunotherapy phase I/II study of ^{131}I-mAb A33 demonstrated that ^{131}I-mAb A33 had modest anticancer effects in heavily pre-treated patients who were no longer responding to chemotherapy. See, for example, Welt et al., *J. Clin. Oncol.* 12:1561-1571 (1994).

[0012] Other clinical trials and results for A33 mAbs have been described in, for example, Welt et al., "Quantitative analysis of antibody localization in human metastatic colon cancer: a phase I study of monoclonal antibody A33," *J. Clin. Oncol.* 8(11):1894-906 (1990); and Welt et al., "Phase I/II study of iodine 131-labeled monoclonal antibody A33 in patients with advanced colon cancer," *J. Clin. Oncol.* 12(8):1561-71 (1994).

[0013] However, A33 is a marker mainly limited to colon cancer. Two novel members of the A33/JAM family are herein described. One new protein/gene is termed "A34." Yet another novel member of this family is also described and is termed "A33-like 3."

[0014] U.S. Patent No. 6,312,921, to Jacobs et al. for "Secreted Proteins and Polynucleotides Encoding Them," discloses protein and polynucleotides with some overlap with A34. However, these sequences are not identical to A34 or A33-like 3; and, in contrast to the disclosed methods of the instant invention, Jacobs' disclosed uses are non-specific, i.e., for unspecified biological activity, research uses, and nutritional uses.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

[0015] Bispecific antibodies: Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for A34 or A33 like 3 , the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

[0016] Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, Nature, 305:537-539 (1983)]. It is also well known within the art of how to generate bispecific antibodies, or bispecific antibody fragments, by using recombinant DNA techniques [Kriangkum et al. Biomol Eng. 2001 Sep;18(2):31-40].

[0017] Cancer: Any one of a number of diseases characterized by uncontrolled cell growth and/or proliferation. Examples are neoplasms, adenocarcinomas, carcinomas, tumors, leukemias, etc.

[0018] CDR: Complementarity determining regions, sections of an immunoglobulin molecule. There are typically three CDRs present in each heavy and light chain, respectively.

[0019] Epitope: A portion of a molecule (generally a protein, though it may be any moiety) that is specifically recognized by an immunoglobulin product.

[0020] Fragment: Various fragments of immunoglobulin or antibodies are known in the art, i.e., Fab, Fab_2, $F(ab')_2$, Fv, Fc, Fd, scFvs, etc. A Fab fragment is a multimeric protein consisting of the immunologically active portions of an immunoglobulin heavy chain variable region and an immunoglobulin light chain variable region, covalently coupled together and capable of specifically binding to an antigen. Fab fragments are generated via proteolytic cleavage (with, for example, papain) of an intact immunoglobulin molecule. A Fab_2 fragment comprises two joined Fab fragments. When these two fragments are joined by the immunoglobulin hinge region, a $F(ab')_2$ fragment results. An Fv fragment is a multimeric protein consisting of the immunologically active portions of an immunoglobulin heavy chain variable region and an immunoglobulin light chain variable region covalently coupled together and capable of specifically binding to an antigen. A fragment could also be a single chain polypeptide

containing only one light chain variable region, or a fragment thereof that contains the three CDRs of the light chain variable region, without an associated heavy chain moiety or, a single chain polypeptides containing only one heavy chain variable region, or a fragment thereof containing the three CDRs of the heavy chain variable region, without an associated light chain moiety; and multi specific antibodies formed from antibody fragments, this has for example been described in US patent No 6,248,516. Fv fragments or single region (domain) fragments are typically generated by expression in host cell lines of the relevant identified regions. These and other immunoglobulin or antibody fragments are within the scope of the invention and are described in standard immunology textbooks such as Paul, *Fundamental Immunology* or Janeway et al. *Immunobiology* (cited above). Molecular biology now allows direct synthesis (via expression in cells or chemically) of these fragments, as well as synthesis of combinations thereof. A fragment of an antinody or immunoglobulin can also have bispecific function as described above.

[0021] Immunoglobulin molecule (Igs): A class of protein molecules present in bodily fluids (e.g., plasma, colostrum, and tears) which have one or more immunoglobulin domains. Typically, a monomeric immunoglobulin molecule comprises four polypeptide chains. The four chains are two identical heavy chains and two identical light chains and are linked by disulfide bonds to form the Y-shaped monomeric antibody molecule.

[0022] Immunoglobulin superfamily molecule: A molecule that has a domain size and an amino acid sequence that is significantly similar to immunoglobulin or immunoglobulin domains. This similarity significance is determined via computer program (for example, Align, a program described by Dayhoff et al., *Meth. Enzymol.* 91: 524-545 (1983)). An Align computer program score of less than 3 indicates that the molecule is a member of an immunoglobulin superfamily. Examples include immunoglobulin heavy chains from IgM, IgD, IgG, IgA, or IgE, light chains kappa and lambda, major histocompatability antigens, etc.

[0023] Multimeric protein: a protein containing more than one separate polypeptide or protein chain associated with one another to form a singular protein unit. The units may be the same or different, i.e., homodimers and heterodimers are both encompassed.

[0024] Polypeptide and peptide: A linear series of amino acids connected covalently by peptide bonds between the alpha amino and carboxy groups of adjacent amino acids.

[0025] Protein: A linear series of greater than about 50 amino acids where said amino acids are connected covalently by peptide bonds between the alpha amino and carboxyl groups of adjacent amino acids.

[0026] Therapeutically effective amount: The amount of a composition administered to a patient in need thereof in the course of treatment. The amount and concentration of the active ingredient(s) is within the skill of one of ordinary skill in the medical and biomedical arts, and takes into account such factors as the age, health, weight, height, overall physical condition, disease state, other medications received, etc., of the patient in need of treatment.

[0027] Treatment or treating: A method of inhibiting, reducing, alleviating, and/or ameliorating all or some of the effects of a disease in a patient. Treatment includes the prevention of occurrence of a disease in a patient who is currently not experiencing any symptoms, but who is or who may be at risk for the disease.

[0028] The instant invention comprises isolated A34 and A33-like 3 proteins and/or polypeptide molecules, and isolated polynucleotide molecules encoding these proteins and/or polypeptide molecules. It also encompasses the isolated immunoglobulin products that bind these proteins and/or any epitopes thereof, and various fragments thereof, including variable regions and/or CDRs.

[0029] The protein and/or immunoglobulin product according to the invention may be isolated from natural sources, or may be produced

recombinantly in host cells. Included within the scope of the invention are the conservative substitutions known to one of ordinary skill in the art, i.e., substitutions resulting in substantially similar sequences. Conservative substitutions are those amino acid or nucleic acid substitutions which do not significantly change the properties of the molecule compared to the molecule before the substitution(s). Substantially similar nucleic acid fragments of the instant invention may also be characterized by the percent identity of the amino acid sequences that they encode to the amino acid sequences disclosed herein, as determined by algorithms commonly employed by those skilled in this art.

[0030] As used herein, the term "conservative substitution" denotes the replacement of an amino acid residue by another, biologically similar residue. As such, it should be understood that in the context of the present invention, a conservative substitution is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Examples of conservative substitutions include the substitution of one hydrophobic residue such as isoleucine, valine, leucine, alanine, cysteine, glycine, phenylalanine, proline, tryptophan, tyrosine, norleucine or methionine for another, or the substitution of one polar residue for another, such as the substitution of arginine for lysine, glutamic acid for aspartic acid, or glutamine for asparagine, and the like. Neutral hydrophilic amino acids which can be substituted for one another include asparagine, glutamine, serine and threonine. The term "conservative substitution" also includes the use of a substituted amino acid in place of an unsubstituted parent amino acid.

[0031] Exemplary conservative substitutions are set out in the following Table A from WO 97/09433.

Table A: Conservative Substitutions I

SIDE CHAIN CHARACTERISTIC	AMINO ACID
Aliphatic Non-polar	G A P I L V
Polar - uncharged	C S T M N Q

SIDE CHAIN CHARACTERISTIC	AMINO ACID
Polar - charged	D E K R
Aromatic	H F W Y
Other	N Q D E

[0032] Alternatively, conservative amino acids can be grouped as described in Lehninger, (*Biochemistry*, 2nd Ed.; Worth Publishers, Inc. NY:NY (1975), pp.71-77) as set out in the following Table B.

Table B: Conservative Amino Acid Substitutions II

SIDE CHAIN CHARACTERISTIC	AMINO ACID
Non-polar (hydrophobic)	
A. Aliphatic:	A L I V P
B. Aromatic:	F W
C. Sulfur-containing:	M
D. Borderline:	G
Uncharged-polar	
A. Hydroxyl:	S T Y
B. Amides:	N Q
C. Sulfhydryl:	C
D. Borderline:	G
Positively Charged (Basic):	K R H
Negatively Charged (Acidic):	D E

[0033] Exemplary conservative substitutions are set out in the following Table C.

Table C

Conservative Substitutions III

Original Residue	Exemplary Substitution
Ala (A)	Val, Leu, Ile
Arg (R)	Lys, Gln, Asn
Asn (N)	Gln, His, Lys, Arg
Asp (D)	Glu
Cys (C)	Ser
Gln (Q)	Asn
Glu (E)	Asp
His (H)	Asn, Gln, Lys, Arg
Ile (I)	Leu, Val, Met, Ala, Phe
Leu (L)	Ile, Val, Met, Ala,

Original Residue	Exemplary Substitution
	Phe
Lys (K)	Arg, Gln, Asn
Met (M)	Leu, Phe, Ile
Phe (F)	Leu, Val, Ile, Ala
Pro (P)	Gly
Ser (S)	Thr
Thr (T)	Ser
Trp (W)	Tyr, Phe
Tyr (Y)	Trp, Phe, Thr, Ser
Val (V)	Ile, Leu, Met, Phe, Ala

[0034] If desired, the peptides of the invention can be modified, for instance, by glycosylation, amidation, carboxylation, or phosphorylation, or by the creation of acid addition salts, amides, esters, in particular C-terminal esters, and N-acyl derivatives of the peptides of the invention. The peptides also can be modified to create peptide derivatives by forming covalent or noncovalent complexes with other moieties. Covalently-bound complexes can be prepared by linking the chemical moieties to functional groups on the side chains of amino acids comprising the peptides, or at the N- or C-terminus.

[0035] In particular, it is anticipated that the aforementioned peptides can be conjugated to a reporter group, including, but not limited to a radiolabel, a fluorescent label, an enzyme (e.g., that catalyzes a colorimetric or fluorometric reaction), a substrate, a solid matrix, or a carrier (e.g., biotin or avidin).

[0036] Suitable nucleic acid fragments (isolated polynucleotides of the present invention) encode polypeptides that are at least about 70% identical, preferably at least about 80% identical, to the amino acid sequences reported herein. Preferred nucleic acid fragments encode amino acid sequences that are about 85% identical to the amino acid sequences reported herein. More preferred nucleic acid fragments encode amino acid sequences that are at least about 90% identical to the amino acid sequences reported herein. Most preferred are nucleic acid fragments that encode

amino acid sequences that are at least about 95% identical to the amino acid sequences reported herein. Suitable nucleic acid fragments not only have the above identities but typically encode a polypeptide having at least 50 amino acids, preferably at least 100 amino acids, more preferably at least 150 amino acids, still more preferably at least 200 amino acids, and most preferably at least 250 amino acids. Also encompassed in the invention are antisense sequences of the isolated polynucleotides of the present invention.

[0037] Sequence alignments and percent identity calculations may be performed, for example, using the Megalign program of the LASERGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Multiple alignment of the sequences may be performed using the Clustal method of alignment (Higgins and Sharp (1989) CABIOS. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments using the Clustal method may be KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5, for example.

[0038] For the multiple sequence alignments shown, the Clustal (found at http://clustalw.genome.ad.jp/) default settings were utilized which rely on a GAP OPEN PENALTY =10 and a GAP EXTENSION PENALTY =0.05. For the pairwise alignments shown, the default settings for BLAST (found at http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html) were used, which rely on a GAP OPEN PENALTY =11 and a GAP EXTENSION PENALTY =1.

[0039] A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually, by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. *J. Mol. Biol.* 215:403-410 (1993); see also www.ncbi.nlm.nih.gov/ BLAST/).

[0040] In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers.

[0041] Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise A34 and A33-like 3. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Figures and Sequence Listing, as well as substantial portions of those sequences as defined above, and antisense sequences thereof.

[0042] "Codon degeneracy" refers to divergence in the genetic code permitting variation of the nucleotide sequence without affecting the amino acid sequence of an encoded polypeptide. Accordingly, the instant invention includes any nucleic acid fragment comprising a nucleotide sequence that encodes all or a substantial portion of the amino acid sequences set forth herein. The skilled artisan is well aware of the "codon-bias" exhibited by a specific host cell in usage of nucleotide codons to specify a given amino acid. Therefore, when synthesizing a nucleic acid fragment for improved expression in a host cell, it is desirable to design the nucleic acid fragment

such that its frequency of codon usage approaches the frequency of preferred codon usage of the host cell.

[0043] The immunoglobulin molecule may be an antibody, an Fv fragment, an F_c fragment, an F_d fragment, a Fab fragment, a Fab' fragment, a $F(ab)_2$ fragment, $F(ab')_2$ fragment, an scFvs fragment, a single chain antibody, a multimeric antibody, or any combination thereof. The immunoglobulin molecule may be joined to a reporter or chemotherapeutic molecule, or it may be joined to an additional fragment, and it may be a monomer or a multimeric product. The immunoglobulin molecule may also be made recombinantly, to include all or part of the variable regions and/or CDRs.

[0044] The inventive protein(s)/antibody(ies) make it possible to detect A34 and/or A33-like 3 polypeptide or polynucleotide molecules, in order to provide a patient with an accurate diagnosis of the presence of cancer that expresses any of these proteins. Detection methods and kits according to the invention may detect A34 and A33-like 3 molecules in any way known in the art. For example, the expression of A34 and A33-like 3 may be detected directly, via mRNA or antisense technology, e.g., by using PCR based techniques, or agents which bind the expressed protein may be detected, e.g., directly with an antibody or polypeptide fragment which binds said A34 and A33-like 3 molecule to form a complex. The antibody or polypeptide fragment which is capable of forming a complex may be linked with a label in order to facilitate detection of the complexes. Such labels are well known in the art, and include, for example, radioactive labels and fluorescent labels.

[0045] The bound complexes comprise immunoglobulin molecules with an affinity for A34 protein. This affinity may be greater than about 50nM, or preferably greater than about 5nM, as measured, for example, by surface plasmon resonance (Biacore™) or other biosensor system.

[0046] The present invention encompasses methods of diagnosing cancer characterized by the presence of A34 antigen in cancer cells, comprising: obtaining a sample of cells of interest; contacting said sample with an agent,

which specifically binds A34 antigen, such that A34/agent complexes may be formed; and detecting the presence or absence of said complexes, wherein the presence of said complexes indicates a positive cancer diagnosis.

[0047] In another embodiment, the present invention encompasses methods for determining regression, progression, or onset of a cancerous condition comprising monitoring a sample from a patient with said cancerous condition for the presence, absence, or change in expression level of A34 antigen comprising: obtaining a sample of interest; contacting said sample with at least one agent, which specifically binds A34 antigen, such that A34/agent complexes may be formed; and detecting the presence, absence or change in of said complexes, wherein the presence, absence, or change in expression level of said complexes indicates progression, regression or onset of cancer diagnosis.

[0048] In a further embodiment, the present invention encompasses methods for determining if cancer cells which express A34 are present in a sample, comprising: contacting a sample of interest with at least one oligonucleotide molecule which specifically hybridizes to a nucleic acid molecule which encodes A34, wherein hybridization of said at least one oligonucleotide molecule to a nucleic acid molecule is indicative of cancer cells which express A34 in said sample; and detecting the presence or absence of such hybridization, wherein the presence of said hybridization indicates the presence of cancer cells which express A34.

[0049] A kit according to the invention generally comprises an appropriate agent which forms a complex with at least one of the A34 and A33-like 3 molecules (either polynucleotide or polypeptide molecules) and instructions for the method of forming and detecting complexes in a sample of interest.

[0050] In general, the patient is a mammal; preferably, the patient is a human.

[0051] A further advantage of the immunoglobulin products according to the instant invention is in methods of treatment of cancers or neoplasms

that express A34 and/or A33-like 3 protein. In addition to detecting these cancers, the immunoglobulins of the instant invention may be used to treat or to reduce the effects of said cancers and neoplasms by administration of the inventive immunoglobulin products, either alone, with a pharmaceutically acceptable carrier, or in combination with another anti-cancer agent. When the inventive immunoglobulin products are administered in combination with an additional anti-cancer agent, the complex is specifically targeted to the cancer cells, thus maximizing the therapeutic potential of the anti-cancer agent while minimizing damage to healthy tissues.

BRIEF DESCRIPTION OF THE DRAWINGS

[0052] The invention will be described in further detail with reference to illustrative embodiments shown in the accompanying drawings.

[0053] Figure 1 shows the end point RT-PCR expression of A34 mRNA in 24 normal tissues.

[0054] Figure 2 shows an analysis of A34 expression in normal and malignant tissues using real-time PCR.

[0055] Figure 3 shows the full length A34 amino acid sequence (SEQ ID NO: 1) and the amino acid sequence comparison of A34 with A33 (SEQ ID NO: 2).

[0056] Figure 4 shows an initially obtained polynucleotide sequence (SEQ ID NO: 3) and amino acid sequence (SEQ ID NO: 4) of A34.

[0057] Figure 5 shows an additional A34 clone polynucleotide (SEQ ID NO: 5) and amino acid sequence (SEQ ID NO: 6).

[0058] Figure 6 shows the polynucleotide sequence (SEQ ID NO: 7) and amino acid sequence (SEQ ID NO: 8) of A33-like 3.

[0059] Figure 7 shows a comparison between the amino acid sequences of A33-like 3 (SEQ ID NO: 9) and A33 (SEQ ID NO: 10).

[0060] Figure 8 shows a Western blot with mAb 342 of normal colonic mucosa and normal gastric mucosa.

[0061] Figures 9 and 10 show immunohistochemical analyses of A34 expression in normal testis.

[0062] Figure 11 shows an immunohistochemical analysis of A34 expression in normal stomach mucosa/surface epithelium.

[0063] Figures 12, 13, and 14 show an immunohistochemical analyses of A34 expression in normal stomach mucosa/fundic glands.

[0064] Figures 15 and 16 show an immunohistochemical analysis of A34 expression in normal pancreas.

[0065] Figures 17-20 show immunohistochemical analyses of A34 expression in stomach carcinoma.

[0066] Figure 21 shows the polynucleotide and amino acid sequences of an murine A34 variable region light chain clone and heavy chain clone designated 209-970. CDRs are indicated with shaded boxes and underlining.

[0067] Figure 22 shows the polynucleotide and amino acid sequences of an murine A34 variable region light chain clone and heavy chain clone designated 209-564. CDRs are indicated with shaded boxes and underlining.

[0068] Figure 23 shows the polynucleotide and amino acid sequences of an murine A34 variable region light chain clone and heavy chain clone designated 209-342.

[0069] Figure 24 shows the amino acid sequences of the CDR regions for the three A34 antibody clones. (SEQ ID NOS: 32-49).

[0070] Figure 25 shows the full length A34 nucleotide sequence, SEQ ID NO: 50.

[0071] Figure 25 shows the full length A34 amino acid sequence, SEQ ID NO 1.

SUMMARY OF THE INVENTION

[0072] The invention relates to novel proteins from the same protein family as the A33 protein and to immunoglobulin products which recognize and bind to these novel proteins. Two additional members of the A33 protein family have been identified and are described herein, i.e., A34 and A33-like 3 protein. All three are members of the A33/JAM family, as shown by their amino acid sequences and expression profiles. Antibodies to A34 are of particular interest in treating esophaegeal, ovarian, and stomach cancers.

EXAMPLE 1

[0073] General Materials and Methods for Reverse Transcription and PCR

[0074] Tumor tissues were obtained from Memorial Sloan-Kettering Cancer Center, Weill Medical College of Cornell University and Aichi Cancer Center Research Center, Nagoya Japan. Normal tissue RNA preparations were purchased from Clontech Laboratories Inc. (Palo Alto, CA) and Ambion Inc. (Austin, Texas). Total RNA from tumor tissues was prepared by the guanidinium thiocyanate method.

[0075] Normalized cDNA preparations derived from various normal tissues were purchased from Clontech laboratories Inc. (Palo Alto, CA). Additional cDNA preparations (tumor and normal tissues) were prepared using the Superscript First strand synthesis kit from Invitrogen Life Technologies (Carlsbad, CA) as per manufacturer's instructions using 5 micrograms of total RNA in 40 ml reaction. Normal tissue cDNA was also purchased from Origene Technologies Inc. (Rockville, MD). This is the source of cDNA panel of 24 tissues used in the end point RT-PCR data shown in Figure 1.

[0076] The concentration of A33, A34 and A33-like 3 mRNA transcripts in normal tissues was measured by real-time RT-PCR using 16 different normal tissue cDNA preparations (ovary, leukocyte, prostate, spleen, testis, thymus, brain, heart, kidney, liver, lung, placenta, skeletal muscle, pancreas, small intestine and colon) that had been normalized for 6

housekeeping genes (Clontech). Gene-specific TaqMan probes and PCR primers were designed using Primer Express software (Applied Biosystems, Foster City, CA), and their sequences are provided below.

[0077] Multiplex PCR reactions were prepared using 2.5 μl of cDNA diluted in TaqMan PCR Master Mix supplemented with 1.25 μl of Vic labeled human beta glucuronidase (GUS) endogenous control probe/primer mix (Applied Biosystems proprietary dye), 200 nM 6-carboxy-fluorescein labeled gene-specific TaqMan probe, and a 900nM concentration of gene specific forward and reverse primers (300-900nM). Triplicate PCR reactions were prepared for each cDNA sample. PCR consisted of 40 cycles of 95°C denaturation (15 seconds) and 60°C annealing/extension (60 seconds).

[0078] Thermal cycling and fluorescent monitoring were performed using an ABI 7700 sequence analyzer (Applied Biosystems). The point at which the PCR product is first detected above a fixed threshold, termed cycle threshold (Ct), was determined for each sample. The abundance of gene-specific transcripts in normal tissues was determined by comparison with a standard curve generated from the Ct values of known concentrations of plasmid DNA template encoding, for example, A33, A34 and/or A33-like 3.

[0079] The quantity of the specific transcripts of interest (i.e., A34, A33-like 3, etc.) present in various cancer specimens and additional normal tissues (breast, stomach, esophagus, cervix, adrenal) were calculated relative to a similarly prepared normal testis cDNA specimen. In these experiments, the resultant Ct values were first normalized by subtracting the Ct value obtained from the GUS endogenous control (DCt = Ct FAM - Ct VIC).

[0080] The concentration of the mRNA of interest (i.e., A34, A33-like 3, etc.) in various cancer specimens and additional normal tissues (experimental samples) was calculated relative to normal testis by subtracting the normalized Ct values obtained with normal tissue (for A34, subtracting the normalized Ct values obtained with normal testis) from

those obtained with experimental samples (DDCt = DCt of experimental samples - DCt of normal tissue), and the relative concentration was determined (Relative Concentration = 2-DDCt, formula derived by Applied Biosystems and published in ABI PRISM 7700 Sequence Detection System User Bulletin #2, 12/11/97).

[0081] Relative concentrations in the experimental samples were then plotted in terms of fg cDNA starting material, using the normalized testis cDNA preparation (Clontech) as a calibrator. For example, A34 mRNA was expressed in gastric cancer specimen #5 at a level that was 0.387 times the level detected in testis, and the expression level of A34 in a normalized, normal testis specimen was equivalent to 3.38 fg of cDNA starting material. Using the expression level in normal testis as a calibrator, gastric cancer specimen #5 was expressed at a level equivalent to 1.31 fg of cDNA starting material (0.387 X 3.38).

EXAMPLE 2

[0082] The A34 gene and its murine orthologue

[0083] Analysis of the human genome database mapped the A34 gene to chromosome Xq22.1-22.3, and revealed no sequences of high similarity, suggesting that A34 is a single copy gene with no additional family members. The A34 gene is approximately 34 Kb in length, equivalent to bp 117203 – 151283 of the chromosome X genomic contiguous sequence, NT 011765. The A34 gene spans 7 exons, whereby exon 1 encodes the 5' untranslated region and a large portion of the signal sequence, exons 2 and 3 encode the variable (V) immunoglobulin (Ig)-like domain, exons 4 and 5 encode the constant type 2 (C_2) Ig-like domain, exon 6 encodes the transmembrane domain and a portion of the cytoplasmic domain, and exon 7 encodes the remainder of the cytoplasmic domain and the 3' untranslated region. This intron/exon structure is quite similar to that of the A33 gene.

[0084] A putative murine ortholog of A34 was identified on the basis of nucleotide similarities, tissue distribution of homologous ESTs, protein

similarities, chromosomal localization, and gene structure. Comparison of the human A34 nucleotide sequence with the mouse EST database showed more than 83% nucleotide identity with EST sequences belonging to murine Unigene cluster Mm.66893. There are currently 31 sequences in this Unigene cluster, including 23 ESTs derived from normal testis, 6 ESTs from derived normal stomach and 2 ESTs from derived normal cecum. This tissue distribution is quite similar to the tissue distribution of human A34 EST sequences.

[0085] The full length murine EST clone, RIKEN cDNA 4930405J24 (Genbank Acc. No. NM_030181), is the reference cDNA sequence for this mouse gene. This transcript consists of 2182 nucleotides and encodes a protein of 407 amino acids, which is 73% identical (330 amino acid overlap) to human A34 and maintains the human A34 domain structure i.e. extracellular V-type and C_2 type Ig-like domains, transmembrane domain, and intracellular domain. The extracellular cysteine residues are conserved among the human and murine proteins, and like human A34, there are 6 potential N-glycosylation sites. The intracellular domain is the least conserved portion of the protein, though, like human A34, EP repeats are also found in carboxyl terminal residues of the intracellular domain of the putative murine protein. The murine A34 gene is approximately 31 Kb in length, equivalent to bp 5534868 – 5566206 of murine chromosome X genomic contiguous sequence, NT 039716, and spans 7 exons, encoding the same protein domains as the 7 exons of human A34 described above.

EXAMPLE 3

[0086] A34 mRNA expression in normal tissues was investigated in an initial experiment by RT-PCR according to the experimental procedure of Example 1 using the following primers:

ACTGTTGGATCTAATGTCAC A33L2F, bp 222 (SEQ ID NO: 11)
AAGGTTTCACTAACACACTG A33L2R, bp 543 (SEQ ID NO: 12)

[0087] The results showed that A34 was expressed in testis and stomach, but no significant expression was found in any of the other 22 normal tissues tested, see Figure 1 (Origene cDNA panel of 24 normal tissues was used).

[0088] Subsequently, a A34 clone of 1045 bp (SEQ ID NO: 5) encoding 348 amino acids (SEQ ID NO: 6) was obtained. Although the protein obtained was partial, its sequence includes all but the amino-terminal-most 48 amino acids (which are part of the extracellular domain) and the caroboxyl-terminal most 48 amino acids (which are part of the intracellular domain).

[0089] Further expression analysis on normal and tumor tissues using real time RT-PCR utilized the following primers:

L2f= GAAGGAGATGGAGCCAATTTCTATT (SEQ ID NO: 13)

L2r= CCTGTAATTCGATCTTTAAATTGCC (SEQ ID NO: 14)

with the following Taqman probe:

6FAM- CTTTTCTCAAGGTGGACAAGCTGTAGCCATC -TAMARA (SEQ ID NO: 15). The experimental procedure was performed similarly to that described in Example 1. In this instance, TAMARA was used as the quencher dye, with VIC or FAM as reporter dyes, though any quencher/reporter system known to one of ordinary skill may also be used.

[0090] This experiment showed significant A34 expression in testis and stomach, while 19 other specimens showed low to trace levels of A34 expression. These results are illustrated graphically in Figure 2. A34 was also expressed at high levels in 2 of 6 gastric cancers, 9 of 16 esophageal cancers, and 4 of 17 ovarian cancers as shown in Table 1. This differential expression can be exploited by targeting with immunoglobulin molecules, such as antibodies, and/or conjugated immunoglobulin molecules, such as antibody-drug conjugates or antibody-radionuclide conjugates for therapeutic or diagnostic purposes. The differential expression can also be exploited for diagnostic purposes by using techniques such as PCR in measuring the A34 nucleic acid expression.

Table 1

Tumor Tissues:	
Gastric Cancer	2/6 (33%)
Esophageal Cancer	9/16 (56%)
Ovarian Cancer	4/17 (23%)
Lung Cancer	0/9
Colon Cancer	0/5
Melanoma	0/3

[0091] Expression profile of A34 mRNA transcripts:

[0092] In order to investigate the expression pattern of A34 mRNA, real-time quantitative RT-PCR was performed using a normalized cDNA panel derived from 21 normal adult tissues, and various malignant tissues. As shown in Figure 2, A34 mRNA was expressed at high levels in testis (3.4 fg) and stomach (7.4 fg), and at a low level in normal pancreas (0.07 fg). Only trace levels (0.03 – 0.001 fg) of mRNA were detected in 13 other normal tissues (spleen, PBL, thymus, brain, heart, liver, lung, placenta, small intestine, breast, esophagus, adrenal gland, cervix). No A34 mRNA was detected in the remaining 5 normal tissues (ovary, prostate, colon, kidney, and skeletal muscle). A34 mRNA expression was also examined in a normalized cDNA panel derived from various malignant tissues. As shown in Figure 2, high level A34 mRNA expression (0.5 fg or above) was detected in 2/6 gastric cancer specimens, 8/16 esophageal cancer specimens, and 4/17 ovarian cancer specimens. A34 mRNA was not detected in lung cancer (0/9 specimens), colon cancer (0/5 specimens), or breast cancer (0/13 specimens). Thus in the cDNA panels examined, A34 mRNA expression was largely restricted to normal testis and stomach, as well as ovarian, gastric and esophageal cancers.

EXAMPLE 4

[0093] Identification of the A34 mRNA transcript:

[0094] In order to identify paralogues of the A33 colon cancer antigen that could serve as novel targets for monoclonal antibody-based therapy of human cancer, the amino acid sequence glycoprotein A33 was compared with a translated, non-redundant nucleotide database:

[0095] (tblastn, http://www.ncbi.nlm.nih.gov/BLAST/). A novel transcript termed A34 was identified, which upon hypothetical translation showed 31% amino acid identity with A33, including limited conservation of a putative signal sequence, immunoglobulin (Ig)-like domains and a transmembrane domain, suggesting it encoded a cell surface protein. The A34 transcript was represented by Unigene cluster Hs.177164 (http://www.ncbi.nlm.nih.gov/entrez), which contains a full length testis-derived cDNA clone, MGC:44287 (Genbank Acc. No. BC043216), as well as 15 other homologous expressed sequence tags (ESTs), derived mainly from normal testis (7 ESTs), and also from normal stomach (2 ESTs), normal aorta (1 EST), uterine cancer (2 ESTs), pancreatic cancer (1 EST), and pooled tissues (2 ESTs). The limited distribution of homologous ESTs suggested that the A34 transcript was differentially expressed.

[0096] Analysis of the human genome database (http://www.ncbi.nlm.nih.gov/ genome) mapped the gene encoding A34 to chromosome Xq22.1. Thus, A34 shares certain characteristics, such as a prevalence of testis-derived ESTs and mapping to chromosome X, with members of the cancer/testis (CT) antigen family, a group of immunogenic proteins whose expression is restricted to gametogenic tissue and cancer, and are considered target molecules for therapeutic cancer vaccines. Therefore, on the basis of its similarity with the A33 colon cancer antigen, the limited tissue distribution of homologous ESTs, and its similarity with CT antigens, the A34 gene product became the focus of our search for novel cell surface molecules expressed in cancer.

[0097] The full length A34 transcript, represented by testis-derived cDNA clone, MGC:44287, consists of 3017 nucleotides (see Figure 25), a length in agreement with the single hybridization signal of 3.1 Kb detected on Northern blots of testis mRNA hybridized with a ^{32}P labeled A34 cDNA probe. The A34 transcript, as represented by MGC:44287, contains 122 bp of 5' untranslated sequence and 1731 bp of 3' untranslated sequence. The A34 nucleotide sequence was verified by sequencing an additional full length A34 EST clone, IMAGE:5266771, as well as four independent cDNA clones, encompassing the entire protein coding region of A34, generated by RT-PCR of human testis RNA. Both strategies yielded cDNA sequences identical to MGC:44287 in the protein coding regions, although IMAGE:5266771 contained a 712 bp deletion in the 3' untranslated region corresponding to nucleotides 1702-2413 of MGC:44287.

[0098] A34 protein:

[0099] An initial experiment showed that A34 (SEQ ID NO: 3) encoded a protein of 387 amino acids (SEQ ID NO: 4). Subsequent cloning of the A34 transcript as detailed above revealed the complete protein and DNA (see SEQ ID NOs: 1 and 50).

[00100] The predicted ATG start site, present at bp 123 of clone MGC:44287, conformed to the Kozak consensus sequence for initiation of protein translation, and is followed by the longest possible open reading frame of 1161 bp. The A34 protein consisted of 387 amino acids (Mr 41,816), comprising three structural domains: an extracellular domain of 233 amino acids, a transmembrane domain of 23 amino acids, and an intracellular domain of 131 amino acids (Figure 3). Following the initial methionine residue, the N-terminal most 21 amino acids formed a putative hydrophobic signal sequence with a possible cleavage site between residues 21 and 22. Amino acid residues 33-123 encompassed an N-terminal, V-type Ig-like domain containing two cysteine residues (C^{43}, C^{116}), which are predicted to form disulfide bonds. A segment of 31 amino acids separated the V-type Ig-like domain from a second Ig-like domain of the C_2 type

present at residues 154-218, which contains two cysteine residues (C^{161}, C^{211}).

[00101] The extracellular domain of A34 has 6 potential N-linked glycosylation sites. Given that the average size of an oligosaccharide chain is approximately of 2.5 kDa, the carbohydrate portion of A34 could potentially contribute approximately 15 kDa of mass, and thus the predicted size of native A34 protein (less the signal peptide of 2.3kDa) is 54.4 kDa. Hydrophobicity plots and transmembrane domain prediction software:

http://sosui.proteome.bio.tuat.ac.jp/sosuiframe0.html and
http://www.cbs.dtu.dk/services/TMHMM/)

located a transmembrane domain at residues 234-256, which was followed by a C-terminal intracellular domain encompasing residues 257-387. The A34 intracellular domain contained 7 sites of potential serine/threonine phosphorylation (casein kinase II phosphorylation sites), and a GSK3 phosphorylation site. Two TRAF2-binding consensus motifs are present at amino acids 314-317 and 324-327. Furthermore, a unique pattern of glutamic acid/proline repeats (EP) is found in the carboxyl terminus of A34. This pattern is found in only two other known human proteins, hematopoietic lineage cell specific protein (HS1) and src substrate protein p85/cortactin.

[00102] The domain organization and amino acid sequence of A34 placed it in the junctional adhesion molecule (JAM) family. The JAM family includes molecules such as GPA33, Coxsackie and adenovirus receptor (CXADR), cortical thymocyte receptor-like protein (CTXL), JAM1/F11 receptor, JAM2, and JAM3/Mac-1 receptor, which are believed to mediate cell-cell adhesion, and localize to tight junctions of epithelial and endothelial cells. Members are characterized by two extracellular Ig-like domains (V and C_2 type), conserved cysteine residues in the extracellular domain, and a single transmembrane domain. The A34 domain structure has a similar organization. An alignment of A34 and A33 is provided in Figure 3. The

A34 amino acid sequence is 35%, 32%, 28%, 26%, 25%, and 27% identical to CTXL (244 amino acid overlap), A33 (262 amino acid overlap), JAM2 (232 amino acid overlap), CXADR (259 amino acid overlap), JAM1 (270 amino acid overlap), and JAM3 (113 amino acid overlap), respectively, with conservation of at least 4/6 cysteine residues in the extracellular domain.

[00103] A34 has a predicted molecular weight of 41.8 kDa and which is 32% identical to A33 and 49% similar to A33, see Table 2 for comparisons with other A33/JAM family proteins (similarity percentage obtained according to BLAST).

[00104] A34 was located in unigene cluster Hs.177164 on chromosome Xq22.1-22.3. The A34 amino acid sequence contains a hydrophilic signal (leader sequence) residues 2-21, two Ig-like domains (residues 33- 123, and 154-218) and a single transmembrane domain (residues 234-256).

Table 2

Family Member Compared with A34	Identity	Similarity	Location
A33	32%	49%	262 aa, A34 aa 1-256, A33 aa 1-257
CXADR	26%	43%	259 aa, A34 aa 9-258, CAR aa 7-261
CTXL	35%	55%	244 aa, A34 aa 9-256, hCTX aa 16-261
ESAM	29%	45%	261 aa, A34 aa 8-254, ESAM aa 16-268
JAM1	25%	40%	270 aa, A34 aa 11-257, JAM1 aa 16-260
JAM2	28%	44%	232 aa, A34 aa 48-258, JAM2 aa 56-262
JAM3	27%	42%	113 aa, A34 aa 158-257, JAM3 aa 3-112

[00105] The intracellular domains of the JAM family, including A34, are poorly conserved. For example, the intracellular domain of A34 consists of

131 amino acids, while the intracellular domain of A33 consists of 60 amino acids, and there is no significant similarity in composition between the two intracellular domains (Figure 3).

[00106] A34 Antibodies:

[00107] In order to investigate the A34 protein *in vivo* and *in vitro*, a murine monoclonal antibodies were generated to the extracellular domain of A34 (amino acids 35-231). A recombinant HIS-tagged recombinant polypeptide, comprising 209 amino acids (23kDa) derived from the extracellular domain of A34, was produced. Mice were immunized with this recombinant polypeptide and three IgG1 monoclonal antibodies were isolated (identified as 342, 564, and 970) and purified in milligram quantities.

[00108] Total RNA was extracted by standard RNA isolation techniques (Chomczynski & Sacchi, *Anal. Biochem.* 1987 162: 156-159) from the hybridomas corresponding to the three IgG1 monoclonal antibodies. First strand cDNA was prepared using the First strand cDNA synthesis kit (Pharmacia Biotech) and priming with d(T)18 for both the heavy and light chains (Renner et al., *Biotechniques* 1998 24(5): 720-2). This cDNA was subjected to PCR using combinations of standard primers for murine heavy and light chains. The PCR products for heavy and light variable regions were cloned using the TA Cloning System (Invitrogen Corporation, Carlsbad, CA) and subsequently sequenced using standard techniques. The sequences for variable and CDR regions of the three murine antibodies are shown in Figures 21-24.

[00109] As shown in Figure 8, monoclonal antibody 342 recognized a 51 kDa protein in Western blots prepared from human gastric mucosa. This protein was not present in similar lysates prepared from human colonic mucosa. The 51 kDa size of the A34 protein detected by Western blotting is consistent with predicted size of 54.4 kDA determined by hypothetical translation of the A34 cDNA and predicted carbohydrate contributions.

[00110] Preliminary immunohistochemical analyses of A34 were done on formalin-fixed paraffin embedded tissues as follows.

[00111] Initially, four antibody clones, which were positive by ELISA, were analyzed by immunohistochemistry (IHC). Reactivity was first tested on frozen tissues with known A34 mRNA expression and different dilutions of newly generated hybridoma supernatant were tested. The tissues were snap-frozen specimens, embedded in OCT (optimal cutting temperature) compound. Five mm cuts were fixed in cold acetone for 10 minutes and blocking of endogenous peroxidase activity was done with 3%H_2O_2. Primary antibody incubation was done overnight at 5°C. The primary antibodies were detected by a biotinylated horse-anti-mouse (Vector, Labs, Burlingame, CA) secondary antibody, followed by an avidin-biotin-complex (ABC-Elite, Vector Labs) system. 3,3'-diaminobenzidine (Liquid DAB, BioGenex, San Ramon, CA) served as a chromogen, and hematoxylin was used as a counterstain.

[00112] Reactive clones were then purified and an optimal working concentration was established by IHC titering on tissue specimens. Three of the four (342, 970, 564) hybridoma clones showed reactivity in frozen stomach and testis, and dilutions were 1:20 of all three clones. These clones were purified and again titered, revealing good staining at 1.0ug/ml.

[00113] In a second step, the three positive clones in frozen tissues were tested on formalin-fixed paraffin embedded (FFPE) tissues blocks using antigen retrieval techniques consisting of a steamer and different antigen retrieval solutions. Incubation and detection of primary antibody was done as with the frozen tissues. A panel of normal tissues as well as gastric carcinomas were analyzed. In formalin fixed parafin embedded tissues, the best staining was achieved by using an antigen-retrieval technique employing heating the slides for 30 minutes at 93°C in an Tris-acetate (TA) buffer solution (pH 8.0, 1mM). All three clones showed similar staining, and 342 was chosen for further analyses.

[00114] Results:

[00115] In normal tissues, immunoreactivity was predominantly present in stomach and testis. In stomach, intense staining was observed in the mucosa. There was mostly membranous and also cytoplasmic staining of all epithelial cellular components reaching from the surface epithelium to the bottom of the specialized glands (Figures 11-14). In testis, a cytoplasmic staining of the germ cells which was present in all tubules could be observed (Figures 9-10). In pancreas, a focal staining of the duct epithelium was occasionally seen (Figures 15-16). No staining was present in any other normal tissue, such as colon, esophagus, small intestine, lung, liver, skin and kidney.

[00116] In a panel of 20 normal tissues, A34 could only be found in stomach mucosa (Figures 11-14), testis (Figures 9-10), and, to a much lesser degree, in pancreas (Figures 15-16). In stomach, the epithelial cells throughout the entire mucosa were stained. No other tissue component was stained. The mucosal cells showed a typical membranous staining pattern. A similar staining pattern was observed in ductal epithelial cells of the pancreas, however, in pancreas, only focal cells were immunopositive.

[00117] In testis, a reactivity staining pattern was observed consisting entirely of germ cells. No staining was observed in the testicular interstitial tissue.

[00118] In a limited set of gastric, ovarian and esophageal carcinomas, A34 showed a mostly heterogeneous or sometimes homogeneous labeling of tumor cells. As in normal tissues, the immunoreactivity pattern was membranous.

[00119] The following tables represent, in tabular form, immunohistochemical analyses performed on gastric/stomach cancer cells, ovarian cancer cells, and esophageal carcinoma cells with A34 clone 342. "Neg" indicates a negative response and the plus signs indicate the percentage of stained tumor cells, where Focal: ~ <5% (for very small

numbers of cells); +: >5-25%; ++ >25-50%; +++ >50-75%; and ++++ >75%. This grading is reproducible and conforms to standard procedures found in the literature.

Table 3: Gastric/stomach cancer

Sample	A34 staining
1	neg
2	neg
3	neg
4	++
5	neg
6	neg
7	neg
8	neg
9	Foc. (single cells)
10	neg
11	Foc. w
12	neg
13	pos
14	Foc. w
15	neg
16	neg
17	Foc.
18	neg
19	Foc.
20	neg.
21	Foc.
22	Neg.
23	neg
24	neg
25	neg
26	neg
27	neg
28	neg
29	neg
30	neg
31	+
32	+++
33	neg
34	neg
35	+
36	++
37	+
38	neg
39	neg
40	neg
41	++++
42	neg
43	+
	Total 14/43 **Foc 6** **+ 4** **++ 2** **+++ 1** **++++ 1**

Table 4: Ovarian cancer

Sample	A34
1	Neg

Sample	A34	
2	Neg	
3	+	
4	Neg	
5	Neg	
6	Neg	
7	Neg	
8	Neg	
9	Neg	
10	++++	
11	Neg	
12	Neg	
13	Neg	
14	Neg	
15	Neg	
16	Neg	
17	Neg	
18	Neg	
19	Neg	
20	Neg	
21	Neg	
	Total	**2/21**
	foc	**-**
	+	**1**
	++	**-**
	+++	**-**
	++++	**1**

Table 5: Eosphaegeal carcinoma

Sample	A34 staining	
1	-	
2	-	
3	+	
4	++	
5	-	
6	-	
7	+	
8	++	
9	++	
10	++	
11	+	
	Total 7/11	
	Neg	**4**
	Foc	**-**
	+	**3**
	++	**4**
	+++	**-**
	++++	**-**

[00120] Table 6 indicates the immunohistochemical analyses of A34 protein expression in normal tissues as detected by A34 antibody clone 342. The majority of the tissues tested were negative. Stomach and testis were positive.

Table 6

Tissue	A34 Clone 342
Esophagus m 2x	-
Esophagus sub 2x	-
Stomach 1x	Pos
Stomach sub 1x	-
Small intestine duo m 1x	-
Small intestine duo sub 1x	-
liver	-
Small intestine m 2x	-
Small intestine sub 2x	-
Colon m 3x	-
Colon sub 3x	-
Appendix m 3x	-
Appendix sub 3x	-
Liver 3x	
Gall bladder	Brownish hue
Pancreatic islets 3x	-
Pancreatic exo 3x	Duct epi.cut/hit in 1 pan
Mesentery	-
Thyroid	-
Synovia	-
Salivary gland 2x	-
Skeletal muscle 3x	-
Synovia	-
Adrenal gland med 4x	-
Adrenal gland cortex 4x	-
Lymph node 1x	-
Peripheral nerve 1x	-
Thymus 2x	-
Spleen 3x	-
Tonsil 3x	-
Lung alve 3x	-
Lung bro 2x	-
Pleura 2x	-
Prostate 2x	GC/ surface
Kidney med 3x	-
Kidney cort 3x	-
Ureter 2x	-
UB m 3x	-
UB sub 3x	Muscl. Pos 1x
Testis 3x	Pos
Vagin 1x	-
Omentum 1x	-
Cervix 2	-
Endometrium 3x	-
Fallopian tub 2x	-
Ovary 3x	-

Tissue	A34 Clone 342
Placenta villi 2x	-
Placenta plate 2x	-
Placenta am = pl 1x	-
Amnion 2x	-
Breast gland 3x	-
Breast duct 3x	-
Skin epithelium 3x	-
Skin dermis 3x	-
Valve 1x	-

EXAMPLE 5

[00121] The stomach/testis-related expression profiles of both human and mouse A34 transcripts suggested that expression of these two orthologs may be under the control of similar regulatory sequences in their corresponding promotors. A comparison of DNA sequences located upstream of the human and mouse A34 start site revealed 64% nucleotide identity between the orthologous genes at positions 1 to 600 of the putative start site (80% identity from 1 to 300 of the putative start site). These regions may constitute the A34 promotor regions.

[00122] Like the human and mouse A33 gene, these putative A34 promotors lack a TATA box within 25-30 bp of the start site, indicating that mRNA transcription is independent of TATA sequences, but do contain a CAAT box, located at position 67 and 70 upstream of the human and murine ATG start site, respectively. Binding sites for 3 tissue specific transcription factors are highly conserved between the human and mouse A34 orthologs, including an intestinal specific homeobox transcription factor, CDX1, and 2 testis-related transcription factors, SRY and SOX-5. CDX1 binding sites, which are also found in the A33 orthologues, are present at 236 and 233 upstream of the human and murine ATG start site, respectively. Binding sites for the 2 testis-related transcription factors, SRY and SOX-5, overlap each other, and are found at positions 294 and 288 upstream of the human and murine ATG start site, respectively. The presence of binding sites for

these 3 transcription factors in the putative A34 promotors is consistent with the stomach/testis-related mRNA expression profile of A34.

[00123] Human A34 promotor region:

[00124] GGTAGTGACAACTGCCAGTGTTTCAAAAAAGAGTAACATATCC AGAGTTTGTTCACACAGAAATGAATGCTTTTTAGCTTCATAACCCCTGT GCCCTTCCCGTGAGCCCCATCTCCCCAGGAAACGATATAGTACCAATTT ACTAACTTAATTTGTAAAAGGAGGTTAGTGAATCAATTCTGTAAGACTC ATGGAAATATTTGAAATTAATTAGCCTTGTCAGCTTTTATTTGCATAGG CTCTCTTCCAACCATATCCCCCAGCCCAAGTACAACGTTTTAGTAAGAT TGATTTTAAACAATGAGACTTAGAGAATCTGTGTACAAGGAGCTTGAAT AATTTAAATGCGTGGGTTTATTATTAACACAGTAGCAAATATATCAAGG AAACACGCCCCATGAAAAGTGTTTCAAAGAAACACAAATCTGTACTGAA AAAAGTCTATACGCAATAAGTAAGCCCAAAGAGGCATGTTTGCTTGGC GATGCCCAGCAGATAAGCCAGGCAAACCTCGGTGTGATCGAAGAAGCC AATTTGAGACTCAGCCTAGTCCAGGCAAGCTACTGGCACCTGCTGCTCT CAACTAACCTCCACACAATG (SEQ ID NO: 16)

[00125] Murine A34 promotor region:

[00126] GGATTTGCTGACAGTCCAATCACTGGAAAGTGTTACTGGAAAT GCCTTATTAGAGTTGAGATTTTTAGCCTGGGACTGGTACAAATTATTAC ATAGGATGAAGGAGAAAGAAACCCAGGAGACCATTCAGGAAGCTGTTG CTTTAGGCTAACGTAATATCTAGAACAAAATGGAAGCAGCAGGTTGGA GATGGGACAAATCTACCATTCACTTTAGAAGCAGCAGGACCAAGATAT CTTATGGGAAGAACTGGAGGAGGCCCTCCAAGTACAACTTTCTTTTTTT AAAAAGGGTTGATTTTAAACAATGTAACCTAAGAGAATCTGTGTACAAA GAACTGAAAGGATTTAAGTGCGTGGTTTATTATTAACACAGTAGCAAAT ATATCAAGGGGACACACCCCGGGGGAAAAGGGTTTCAAATAAACACAG ATTTGTTCAGAGAGAACTCAGTGCCCAATAAGCAAGCGTAAGGAGGCC TATTTGCTTGGTGATGCCCAGCCGATAAGCCAGGCTGTGACTGAAGAA GCCAATTTGAAACTCAGCCTAGTTCAGGCAGCCTTCGGACTGGCACCT GCTGCTCCAAGCGACTTTCAGCATG (SEQ ID NO: 17)

[00127] The ATG start codon is underlined in the murine and human sequences.

EXAMPLE 6

[00128] A33-like 3 (SEQ ID NO: 7) is located on human chromosome 1 at >gi|18547605|ref|XM_089096.1|, and has similarities with coxsackievirus and adenovirus receptor-like proteins. A33-like 3 polypeptide molecule (SEQ ID NO: 8) weighs approximately 40,085 Da (approx. 370 amino acids) which is 27% identical to A33 and 40% similar to A33 (using computer-based sequence comparison and identification tools that employ algorithms, i.e., BLAST or a similar program).

[00129] A33-like 3 protein has one transmembrane domain, extending from amino acids 4-26, and has two Ig-like domains extending from amino acids 37-128 and 160-241. Table 7 shows a comparison between A33-like 3 and the other family members, including the novel polypeptide A34.

Table 7

Family Member Compared with A33-like 3	Identity	Similarity	Location
A33	27%	40%	232 aa, A33-like 3 aa 29-256, A33 aa 28-228
CAR	33%	49%	231aa, A33-like 3 aa 29-256, CAR aa 26-229
HCTX	23%	42%	168 aa, A33-like 3 aa 95-258, hCTX aa 109-255
ELAM	25%	40%	168 aa, A33-like 3 aa 97-257, ELAM aa 100-244
JAM1	24%	33%	219 aa, A33-like 3 aa 34-246, JAM1 aa 40-219
JAM2	28%	36%	150 aa, A33-like 3 aa 108-250, JAM2 aa 91-225
JAM3	none	none	n/a
A34 (A33-like 2)	24%	45%	161 aa, A33-like 3 aa 101-257

[00130] A33-like 3 mRNA expression in normal tissues is investigated in an initial experiment by RT-PCR according to the experimental procedure of Example 1 using the following primers:

TGCCCATGTGCTGGACAGAG, A33L3F, bp 733 (SEQ ID NO: 18)

CACGTTGTTGGCCACTGTGC, A33L3R, bp 1025 (SEQ ID NO: 19)

EXAMPLE 7

[00131] Recombinant protein A34 and A33-like 3, or fragments thereof, are produced from the appropriate isolated cDNA sequence. Mic, rabbits, or other appropriate mammals are immunized with at least one of recombinant or isolated A34 protein (either whole or appropriate antigenic fragments), and antibodies are generated and purified by standard techniques as detailed in the references cited previously and known to those of skill in the art.

EXAMPLE 8

[00132] Antibodies targeting the A34 and/or A33-like 3 antigens are used for both diagnostic and therapeutic purposes. For therapeutic purposes the naked (unconjugated) antibody itself is used as a therapeutic, for example, by eliciting a immunoresponse against a tumor by stimulating ADCC and/or CDC responses. The A34 and/or A33-like 3 specific antibodies are conjugated with a radioisotope or a chemotherapeutic or cytotoxic agent for both therapeutic and/or diagnostic purposes. The radioisotope is, for example, ^{125}I, ^{131}I, ^{99}Tc, ^{90}Y and ^{111}In, or any other γ, α or β emitter. Those of skill in the art will appreciate that many methods are suitable for the conjugation of an antibody with a radioisotope, e.g., U.S. Patent Nos. 5,160,723 and 5,851,526.

[00133] The antibodies that bind to A34 and/or A33-like 3 antigens are optionally conjugated with at least one chemotherapeutic agent, or at least one cytotoxic agent, or may be used in conjunction with such an agent. For

example, the antibodies can be conjugated to, or used in combination therapy together with, QFA (an antifolate), BCNU, mercaptopurine, methotrexate, docetaxel, adriamycin or calicheamicin. These are all well known chemotherapeutics or cytotoxic drugs and conjugation, and combination use, of these with proteins, including antibodies, have been described, e.g. Hellstrom et al., *Methods Mol. Biol.* 166:3-16 (2001); Sievers et al., *Curr. Opin. Oncol.* 13(6):522-7 (2001); Winer et al., *Oncology* 61 Suppl 2:50-7 (2001).

[00134] The antibodies, or any fragments thereof, may also be conjugated or recombinantly fused to any cellular toxin, bacterial or other, e.g., pseudomonas exotoxin, ricin, or diptheria toxin. The part of the toxin used can be the whole toxin, or any particular domain of the toxin. Such antibody-toxin molecules have successfully been used for targeting and therapy of different kinds of cancers, see e.g., Pastan, *Biochim Biophys Acta.*, 1333(2):Cl-6 (Oct. 24, 1997); Kreitman et al., *New Engl. J. Med.* 345(4):241-247 (2001); Schnell et al., *Leukemia* 14(1):129-35 (2000) and Ghetie et al., *Mol. Biotechnol.*, 18(3):251-68 (2001).

[00135] Other conjugation partners can also be conjugated to the antibodies used in the methods of this invention, for example, enzymes, and prodrugs, such as the ADEPT approach, e.g., Xu et al., *Clin Cancer Res.* 7(11):3314-24 (2001). Any method known in the art for preparing antibody conjugates may be used to generate conjugates useful in this invention. The A34 or A33-like 3 specific antibodies conjugated with a cytotoxic or chemotherapeutic agent may be administered to a patient in need thereof before, after, or concurrently with a non-conjugated form of an A34 or A33-like 3 specific antibody.

[00136] Examples describing drug conjugates, etc. are found in: Hellstrom et al., "Development and activities of the BR96-doxorubicin immunoconjugate," *Methods Mol Biol.*166:3-16 (2001); Sievers et al., "Mylotarg: antibody-targeted chemotherapy comes of age," *Curr Opin Oncol.* 13(6):522-7 (2001); Winer et al., "New combinations with Herceptin in

metastatic breast cancer," *Oncology* 61 Suppl 2:50-7 (2001); Pastan I., "Targeted therapy of cancer with recombinant immunotoxins," *Biochim Biophys Acta.*1333(2):C1-6 (1997); Kreitman et al., "Efficacy of the anti-CD22 recombinant immunotoxin BL22 in chemotherapy-resistant hairy-cell leukemia," *New Engl J. Med.* 345(4):241-7 (2001); Schnell et al., "Treatment of refractory Hodgkin's lymphoma patients with an anti-CD25 ricin A-chain immunotoxin," *Leukemia* 14(1):129-35 (2000); Ghetie et al., "Chemical construction of immunotoxins," *Mol Biotechnol.* 18(3):251-68 (2001); Xu et al., "Strategies for enzyme/prodrug cancer therapy," *Clin. Cancer Res.* 7(11):3314-24 (2001); Hudson et al., "Recombinant antibodies for cancer diagnosis and therapy," *Expert Opin Biol Ther.* 1(5):845-55 (2001).

EXAMPLE 9

[00137] Humanized, fully human, and/or chimeric antibodies and/or immunoglobulin products which bind to A34 and/or A33-like 3 are used as targeting agents in conjunction with other cancer therapies. The antibody, fragment, or other immunoglobulin product is linked to an additional anti-cancer agent, and a therapeutically effective amount of the conjugate produced is administered to a patient in need thereof. Alternatively, the agent is linked to a label for detection. Examples of labels include radioactive isotopes and fluorescent markers. The linkage may be covalent or ionic in nature.

EXAMPLE 10

[00138] These antibodies, or antigenically active fragments thereof which bind to A34 and/or A33-like 3 are further manipulated by molecular biological techniques known in the art to make humanized antibodies. The antibodies may be fully or partially human.

EXAMPLE 11

[00139] Humanized, fully human, and/or chimeric antibodies and/or immunoglobulin products which bind to A34 and/or A33-like 3, or appropriately antigenic fragments that bind to at least one of A34 and A33-like 3, are combined with, or linked to, other agents, such as radioisotopes, chemotherapeutic agents, cytokines, cytotoxic agents, or other immunoglobulin products. The linkage may be ionic or covalent, and is formed by methods known in the art (see references cited above).

EXAMPLE 12

[00140] A composition of at least one immunoglobulin product (whether an antibody, a fragment, or an immunoglobulin linked to another agent, or any combination thereof), wherein said at least one immunoglobulin product binds to at least one of A34 and/or A33-like 3, will be formed by combining a therapeutically effective amount of said immunoglobulin product with a pharmaceutically acceptable carrier. This composition will then be administered to a patient in need thereof (i.e., a human or other mammal).

[00141] Such patients will be suffering from a disorder, such as a neoplastic disease, wherein the disorder expresses the antigen to which the immunoglobulin product binds (i.e., A34 or A33-like 3).

[00142] A composition, or treatment regimen, with at least one immunoglobulin product (whether an antibody, a fragment, or an immunoglobulin linked to another agent, or any combination thereof), wherein said at least one immunoglobulin product binds to at least one of A34 and/or A33-like 3, will be formed by combining said immunoglobulin product with a chemotherapeutic agent. The chemotherapeutic agents may be administered prior to, concurrently with, or after A34 and/or A33-like 3 specific immunoglobulin product is administered to the patient. Examples of chemotherapeutic drugs that could be used in such a combination are (but not limited to) oxaliplatin, irinotecan, topotecan, carmustine, vincristine, leucovorin, streptozocin, Orzel™ and fluoropyrimidines, e.g., 5- fluorouracil,

ftoraflur, capecitabine, gemcitabine, floxuridine and fluoritine, and other nucleoside analogs, and vinca alkaloid analogs, including but not limited to vinblastine, navelbine, and vinzolidine, topoisomerase I inhibitors, including but not limited to topotecan and camptothecin, and other platinum analogs including but not limited to cisplatin and carboplatin.

[00143] A composition, or treatment regimen, with at least one immunoglobulin product (whether an antibody, a fragment, or an immunoglobulin linked to another agent, or any combination thereof), wherein said at least one immunoglobulin product binds to at least one of A34 and/or A33-like 3, is formed by combining said immunoglobulin product with another immunoglobulin product that is not specific for A34 or the A33 like 3 antigens. Examples of such immunoglobulins are antibodies targeting receptors of the Epidermal Growth Factor Receptor (EGFR) family of proteins, e.g., Cetuximab (Erbitux™, ImClone Systems Inc.) and Trastuzumab (Herceptin™, Genentech Inc.).

[00144] A composition, or treatment regimen, with at least one immunoglobulin product (whether an antibody, a fragment, or an immunoglobulin linked to another agent, or any combination thereof), wherein said at least one immunoglobulin product binds to at least one of A34 and/or A33-like 3, is formed by combining said immunoglobulin product with a small molecule signalling inhibitor. Examples of such small molecule signaling inhibitors are Imatinib Mesylate (Glivec®, Novartis AG) and Gefitinib (Iressa™, AstraZeneca Ltd.).

[00145] The foregoing description and examples have been set forth merely to illustrate the invention and are not intended to be limiting. Since modifications of the described embodiments incorporating the spirit and substance of the invention may occur to persons skilled in the art, the invention should be construed broadly to include all variations falling within the scope of the appended claims and equivalents thereof.